electrophoresis of a large number of nucleic acid samples efficiently and detect nucleic acid bands of interest.

Change the paragraph extending from page 16, lines 9 to 11 to read as follows:

In this application, although combination of n bands enables identification of up to 2n breeds/lines theoretically (where n is an integer), it may be slightly less than that practically.

Change the paragraph extending from page 21, line 31 to page 22, line 14 to read as follows:

To achieve almost one-to-one correspondence between the AFLP bands and the library clones, the genomic library for the entire genome, which generally has several genome equivalents or more, is divided into several sublibraries of approximately 1 genome equivalent each. Each component clone of the sublibraries is uniquely identified by coordinate of row, column, and plate numbers of the microplate. Therefore, using row, column, and plate numbers as coordinate axes, small amounts of DNAs are collected from groups of clones with a common axis coordinates, and mixed to provide coordinate samples representing positions on each axis. By performing genome scanning of the present invention using these coordinate samples as templates and comparing AFLP patterns with control lanes, which are prepared by using whole genome DNA as templates, placed on both sides of the coordinate lanes, clones corresponding to specific bands from the genomic DNA templates are readily detected from the sublibrary. When there are 2 to n corresponding clones in the sub-group (where n is an integer), $2^3 = 8$ to n^3 clones correspond to the bands. In this case, by removing these 8 clones and performing second electrophoresis of the genome scanning method, the truly corresponding 2 clones are identified. Specific procedures to prepare coordination samples of a sublibrary are shown in Example 5.

In the Claims:

Please amend claims 5, 9, 11, 13, and 15 as follows:

5.   The method according to claim 1, wherein the method is performed in order to detect a polymorphism of genomic DNAs among test individuals.